

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 12:18:43 ; Search time 15.09 seconds
(without alignments)
101.884 Million cell updates/sec

Title: US-09-832-510-2

Perfect score: 86

Sequence: 1 XRRRAVDTCRHNIGV 16

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match	Length	DB	ID	Description
1	85	98.8	51	2	D25239		MHC class II histo
2	85	98.8	74	2	I68827		MHC class II HLA-D
3	85	98.8	75	2	I34309		major histocompati
4	85	98.8	78	2	I54528		MHC class II HLA-D
5	85	98.8	80	2	S54258		HLA DRB1 protein -
6	85	98.8	82	2	I37539		histocompatibility
7	85	98.8	85	2	B45832		MHC class II histo
8	85	98.8	90	2	B27060		class II histocomp
9	85	98.8	94	2	B30575		MHC class II histo
10	85	98.8	94	2	T01409		HLA-DRB1 protein -
11	85	98.8	94	2	I79419		MHC HLA-DR-beta-1
12	85	98.8	94	2	I79422		MHC HLA-DR-beta-1
13	85	98.8	100	2	G02161		KRAB zinc finger p
14	85	98.8	116	2	I38898		MHC class II histo
15	85	98.8	123	2	A25239		class II histocomp
16	85	98.8	136	2	I38425		gene HLA-DRB1-1113
17	85	98.8	140	2	B28756		class II histocomp
18	85	98.8	193	2	C32526		class II histocomp
19	85	98.8	237	2	B28043		MHC class II histo
20	85	98.8	237	2	F27060		class II histocomp
21	85	98.8	266	1	HLH04D		MHC class II histo
22	85	98.8	266	1	HLH01B		MHC class II histo
23	85	98.8	266	2	I68733		MHC HLA-DR-beta ch
24	85	98.8	266	2	A25324		class II histocomp
25	85	98.8	266	2	B27618		MHC class II histo
26	85	98.8	266	2	I67726		cell surface glyco
27	85	98.8	296	2	S01441		class II histocomp
28	82	95.3	78	2	I59629		lymphocyte antigen
29	82	95.3	88	2	G02057		MHC class II DRB1-

ALIGNMENTS

RESULT 1

D25239

MHC class II histocompatibility antigen HLA-DR-2-DHO-7 beta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 09-May-1997
C:Accession: D25239
R:Wu, S.; Saunders, T.L.; Bach, F.H.
Nature 324, 676-679, 1986
A:Title: Polymorphism of human Ia antigens generated by reciprocal intergenic exchange
A:Reference number: A25239; MUID:87090380
A:Accession: D25239
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-51 <RES>
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTCRHNIGV 16
Db 28 RRAAVDTCRHNIGV 42
|||||

RESULT 2

I68827

MHC class II HLA-DQ-beta-1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I68827
R:Dong, R.P.; Kimura, A.; Sasazuki, T.
Immunogenetics 36, 130-133, 1992
A:Title: Sequence analysis of three novel DRw14-DRB1 alleles.
A:Reference number: I54949; MUID:92307744
A:Accession: I68827
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-74 <RES>
A:Cross-references: GB:M74032; NID:q184221; PIDN:AAA63193.1; PID:q703086
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTCRHNIGV 16
Db 59 RRAAVDTCRHNIGV 73
|||||

30 82 95.3 101 2 I72483 MHC class II histo
31 82 95.3 266 2 A29310 MHC class II histo
32 81 94.2 80 2 I54469 MHC HLA-DR-beta-1
33 81 94.2 80 2 I68777 MHC HLA-DR-beta-1
34 81 94.2 81 2 I54550 HLA DRB1*1202 - hu
35 81 94.2 85 2 I59634 MHC class II histo
36 81 94.2 89 2 S38676 lymphocyte antigen
37 81 94.2 266 2 I54295 lymphocyte antigen
38 80 93.0 73 2 I54516 MHC HLA-DRB1 - hum
39 80 93.0 76 2 I51875 gene HLA-DRB1 prot
40 80 93.0 78 2 I59643 MHC class II HLA-D
41 80 93.0 78 2 I54494 MHC class II HLA-D
42 80 93.0 78 2 I68828 MHC class II histo
43 80 93.0 80 2 A45873 MHC class II histo
44 80 93.0 80 2 I68778 HLA-DR-beta-1 chai
45 80 93.0 80 2 S54907 Beta 1 domain of M

```
RESULT 3
I54309
major histocompatibility complex class II - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I54309
R:Lee, K.W.
Hum. Immunol. 37, 229-236, 1993
A:Title: DR6 in Koreans, DR11 frequently acts as a recipient gene to create DR13 alleles
A:Reference number: I54309; MUID:94131815
A:Accession: I54309
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-75 <RES>
A:Cross-references: GB:L06847; NID:q404720; PIDN:AAA75387.1; PID:g986880
C:Genetics:
A:Gene: HLA-DRB13
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDYCRHNYGV 16
|||||
Db 60 RRAAVDYCRHNYGV 74

RESULT 4
I54528
MHC class II HLA-DR-beta - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I54528
R:Pando, M.; Theiller, G.; Melano, R.; Petzl-Erler, M.L.; Satz, M.L.
Immunogenetics 39, 377, 1994
A:Title: A new HLA-DR6 allele (DRB1*1413) found in a tribe of Brazilian Indians.
A:Reference number: I54528; MUID:94222454
A:Accession: I54528
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-78 <RES>
A:Cross-references: GB:L21755; NID:q347326; PIDN:AAA58657.1; PID:g553345
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDYCRHNYGV 16
|||||
Db 63 RRAAVDYCRHNYGV 77

RESULT 5
S54258
HLA DRB1 protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C:Accession: S54258
R:Murrin, M.R.; Costa, G.; Muntioni, F.; Martos, M.G.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54258
A:Accession: S54258
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-80 <MUR>
A:Cross-references: EMBL:X86803; NID:g804987; PIDN:CAA60498.1; PID:g804988
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
```

```
Query Match 98.8%; Score 85; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDYCRHNYGV 16
|||||
Db 62 RRAAVDYCRHNYGV 76

RESULT 6
I37539
histocompatibility antigen HLA-DR4 beta chain (allele DRB1*0415) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 23-Jul-1999
C:Accession: S60308; I37539
R:tiercy, J.M.; Gebuhrer, L.; Betuel, H.; Mach, B.; Jeannet, M.
Tissue Antigens 41, 97-101, 1993
A:Title: A new HLA-DR4 allele with a DR11 alpha-helix sequence.
A:Reference number: I37539; MUID:93235215
A:Accession: S60308
A:Molecule type: DNA
A:Residues: 1-82 <TIE>
A:Cross-references: EMBL:X68272; NID:g984140; PIDN:CAA48333.1; PID:g984141
A:Note: the sequence of residues 75-82 and the corresponding nucleotide sequence are
C:Genetics:
A:Gene: HLA-DRB1
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDYCRHNYGV 16
|||||
Db 66 RRAAVDYCRHNYGV 80

RESULT 7
B45832
MHC class II histocompatibility antigen HLA-DRB1 (PEV) beta chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
C:Accession: B45832; I79668
R:Petersdorf, E.W.; Griffith, R.L.; Erlich, H.A.; Mickelson, E.M.; Smith, A.G.; Nispe
Immunogenetics 32, 96-103, 1990
A:Title: Unique sequences for two HLA-DRB1 genes expressed on distinct DRw6 haplotype
A:Reference number: A45832; MUID:90375198
A:Accession: B45832
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-85 <PET>
A:Cross-references: GB:M57600; GB:M35183; NID:g188325; PIDN:AAA36292.1; PID:g188326
R:Gyllenstein, U.B.; Sundvall, M.; Erlich, H.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 3686-3690, 1991
A:Title: Allelic diversity is generated by intraexon sequence exchange at the DRB1 lo
A:Reference number: I59196; MUID:91219437
A:Accession: I79668
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-73 <RES>
A:Cross-references: GB:M63216; NID:g181802; PIDN:AAA52325.1; PID:g181803
C:Genetics:
A:Gene: GDB:HLA-DRB1
A:Cross-references: GDB:120642
A:Map position: 6p21.3-6p21.3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2 RRAAVDTYCRHNYGV 16
|||||
Db 66 RRAAVDTYCRHNYGV 80

RESULT 8

B27060
class II histocompatibility antigen HLA-DR2 Dw12a beta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999
C:Accession: B27060
R:Lee, B.S.M.; Rust, N.A.; McMichael, A.J.; McDevitt, H.O.
Proc. Natl. Acad. Sci. U.S.A. 84, 4591-4595, 1987
A:Title: HLA-DR2 subtypes form an additional supertypic family of DR-beta alleles.
A:Reference number: A94165; MUID:87260854
A:Accession: B27060
A:Molecule type: mRNA
A:Residues: 1-90 <LEE>
A:Cross-references: GB:M16955; NID:q188245; PIDN:AAA36277.1; PID:q188246
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
C:Keywords: heterodimer

Query Match 98.8%; Score 85; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
|||||
Db 71 RRAAVDTYCRHNYGV 85

RESULT 9

B30575
MHC class II histocompatibility antigen HLA-DRw14 beta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 18-Apr-1989 #sequence_revision 18-Apr-1989 #text_change 23-Jul-1999
C:Accession: B30575; I39439
R:Kao, H.T.; Gregersen, P.K.; Tang, J.C.; Takahashi, T.; Wang, C.Y.; Silver, J.
J. Immunol. 142, 1743-1747, 1989
A:Title: Molecular analysis of the HLA class II genes in two DRw6-related haplotypes, DR
A:Reference number: A30575; MUID:89140369
A:Accession: B30575
A:Molecule type: DNA
A:Residues: 1-94 <KAO>
A:Cross-references: GB:M25266; NID:g602462; PIDN:AAA57259.1; PID:g602463
R:Gorski, J.
Hum. Immunol. 24, 145-149, 1989

A:Title: First domain sequence of the hla-drbl chain from two hla-drw14 homozygous typin
A:Reference number: I39439; MUID:89174060
A:Accession: I39439
A:Status: translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-94 <RES>
A:Cross-references: GB:M27645; NID:q178515; PIDN:AAA72783.1; PID:q178516
A:Experimental source: AMALA (Dw16) cell line
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
|||||
Db 71 RRAAVDTYCRHNYGV 85

RESULT 10

T01409
HLA-DRB1 protein - human (fragment)
C:Species: Homo sapiens (man)

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C:Accession: T01409
R:O'Brien, R.M.; Cram, D.S.; Russ, G.R.; Starr, R.; Tait, B.D.
Hum. Immunol. 34, 147-151, 1992
A:Title: Nucleotide sequences of the HLA-DRw12 and DRw8 B1 chains from an Australian
A:Reference number: Z14318; MUID:93053838
A:Accession: T01409
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-94 <OBR>
A:Cross-references: EMBL:S48645; NID:g259088; PIDN:AA24005.2; PID:g5705940
C:Gene: HLA-DRB1

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
|||||
Db 71 RRAAVDTYCRHNYGV 85

RESULT 11

I79419
MHC HLA-DR-beta-1 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999
C:Accession: I79419
R:Gregersen, P.K.; Shen, M.; Song, Q.
Proc. Natl. Acad. Sci. U.S.A. 83, 2642-2646, 1986
A:Title: Molecular diversity of HLA-DR4 haplotypes.
A:Reference number: I59062; MUID:86206008
A:Accession: I79419
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-94 <RES>
A:Cross-references: GB:M15069; NID:q188357; PIDN:AAA59809.1; PID:q188360
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
|||||
Db 71 RRAAVDTYCRHNYGV 85

RESULT 12

I79422
MHC HLA-DR-beta-1 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999
C:Accession: I79422
R:Gregersen, P.K.; Shen, M.; Song, Q.
Proc. Natl. Acad. Sci. U.S.A. 83, 2642-2646, 1986
A:Title: Molecular diversity of HLA-DR4 haplotypes.
A:Reference number: I59062; MUID:86206008
A:Accession: I79422
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-94 <RES>
A:Cross-references: GB:M15070; NID:q188366; PIDN:AAA59812.1; PID:q188367
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTYCRHNYGV 16
|||||
Db 71 RRAAVDTYCRHNYGV 85

RESULT 13

G02161
KRAB zinc finger protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: G02161
R:Hurley, C.K.
submitted to the EMBL Data Library, October 1995
A:Reference number: G09254
A:Accession: G02161
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-100 <HUR>
A:Cross-references: EMBL:U37582; NID:gl017836; PIDN:AAA79205.1; PID:gl017837
C:Genetics:
A:Gene: DRB52
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTYCRHNYGV 16
|||||
Db 71 RRAAVDTYCRHNYGV 85

RESULT 14

I38898
MHC class II histocompatibility antigen DR-beta 1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 23-Jul-1999
C:Accession: I38898
R:Robbins, F.; Tang, T.; Yao, H.; Ng, J.; Hartzman, R.J.; Hurley, C.K.
Tissue Antigens 45, 302-308, 1995
A:Title: Direct sequencing of SSP-PCR-amplified cDNA to identify new alleles in the DR52
A:Reference number: I38897; MUID:95381230
A:Accession: I38898
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-116 <RES>
A:Cross-references: EMBL:U17380; NID:g841153; PIDN:AAC50166.1; PID:g841154
C:Genetics:
A:Gene: HLA-DRB1
A:Cross-references: GDB:120642
A:Map position: 6p21.3-6p21.3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTYCRHNYGV 16
|||||
Db 75 RRAAVDTYCRHNYGV 89

RESULT 15

A25239
class II histocompatibility antigen HLA-DR-2-Mn2-61 beta chain precursor - human (fragme
C:Species: Homo sapiens (man)
C:Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_change 23-Jul-1999
C:Accession: A25239
R:Wu, S.; Saunders, T.L.; Bach, F.H.
Nature 324, 676-679, 1986

A:Title: Polymorphism of human Ia antigens generated by reciprocal intergenic exchange
A:Reference number: A25239; MUID:87090380
A:Accession: A25239
A:Molecule type: mRNA
A:Residues: 1-123 <WUS>
A:Cross-references: GB:M30179; GB:X04740; NID:gl88514; PIDN:AAA59842.1; PID:gl88515
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 98.8%; Score 85; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTYCRHNYGV 16
|||||
Db 100 RRAAVDTYCRHNYGV 114

Search completed: July 1, 2002, 12:20:50
Job time: 127 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 12:20:33 ; Search time 10.37 Seconds
(without alignments)
59.741 Million cell updates/sec

Title: US-09-832-510-2

Perfect score: 86

Sequence: 1 XRRRAVDTCRHHYGV 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	85	98.8	266	1 HB2C_HUMAN	P01914 homo sapien
2	85	98.8	266	1 HB2D_HUMAN	P13759 homo sapien
3	85	98.8	266	1 HB2F_HUMAN	P13758 homo sapien
4	85	98.8	266	1 HB2I_HUMAN	P20039 homo sapien
5	82	95.3	266	1 HB2H_HUMAN	P13760 homo sapien
6	80	93.0	198	1 HB2G_HUMAN	P01911 homo sapien
7	76	88.4	232	1 HB23_MOUSE	P04231 mus musculus
8	76	88.4	266	1 HB2K_CANFA	P18470 canis famil
9	74	86.0	266	1 HB2K_HUMAN	P13762 homo sapien
10	73	84.9	264	1 HB2I_MOUSE	P20040 mus musculus
11	73	84.9	264	1 HB2I_MOUSE	P18468 mus musculus
12	68	79.1	264	1 HB22_MOUSE	P01915 mus musculus
13	68	79.1	266	1 HB2A_HUMAN	P01913 homo sapien
14	68	79.1	266	1 HB2B_HUMAN	P01912 homo sapien
15	68	79.1	266	1 HB2E_HUMAN	P04229 homo sapien
16	68	79.1	266	1 HB2J_HUMAN	P04229 homo sapien
17	67	77.9	264	1 HB2J_MOUSE	P18469 mus musculus
18	60	69.8	264	1 HB2I_MOUSE	P04230 mus musculus
19	58	67.4	261	1 HB2I_HUMAN	P01918 homo sapien
20	57	66.3	265	1 HB2Q_MOUSE	P06342 mus musculus
21	56	65.1	261	1 HB25_HUMAN	P03992 homo sapien
22	56	65.1	265	1 HB2D_MOUSE	P01921 mus musculus
23	56	65.1	268	1 HB2X_HUMAN	P05538 homo sapien
24	55	64.0	261	1 HB22_HUMAN	P01919 homo sapien
25	54	62.8	252	1 HB2F_MOUSE	P06346 mus musculus
26	54	62.8	258	1 HB2D_PIG	P15983 sus scrofa
27	54	62.8	261	1 HB23_HUMAN	P05537 homo sapien
28	54	62.8	261	1 HB2A_HUMAN	P01920 homo sapien
29	54	62.8	263	1 HB2B_RAT	P29826 rattus norv
30	54	62.8	263	1 HB2K_MOUSE	P06343 mus musculus
31	54	62.8	263	1 HB2S_MOUSE	P06345 mus musculus
32	54	62.8	265	1 HB2A_MOUSE	P14483 mus musculus
33	51	59.3	257	1 HB2P_RABIT	P20756 coryctolagus

34	51	59.3	258	1 HB2I_SPAEH	P15464 spalax leuc
35	50	58.1	233	1 HB2A_RAT	P06341 rattus norv
36	50	58.1	264	1 HB2D_RAT	P18211 rattus norv
37	50	58.1	273	1 HB2O_HUMAN	P13765 homo sapien
38	50	58.1	273	1 HB2O_PANTR	P18467 pan troglod
39	49	57.0	261	1 HB2C_PIG	P15982 sus scrofa
40	48	55.8	224	1 HB2S_HUMAN	P01916 homo sapien
41	48	55.8	258	1 HB2P_HUMAN	P04440 homo sapien
42	48	55.8	263	1 HB2U_MOUSE	P06344 mus musculus
43	46	53.5	181	1 HB2T_HUMAN	P04232 homo sapien
44	46	53.5	258	1 HB2Q_HUMAN	P13763 homo sapien
45	44	51.2	331	1 DIV_ECOLI	P15286 escherichia

ALIGNMENTS

```
RESULT 1
ID HB2C_HUMAN STANDARD; PRT; 266 AA.
AC P01914;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE HLA class II histocompatibility antigen, DR-1 beta chain precursor
DE HLA class II histocompatibility antigen, DR-1 beta chain precursor
DE (Clone P2-beta-4).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84261468; PubMed=6589154;
RA Larhammar D., Gustafsson G., Wiman K.G., Emmoth E., Larhammar D.,
RA Boelme J., Hyldig-Nielsen J.J., Ronne H., Rask L.;
RT "Mutations and selection in the generation of class II
RT histocompatibility antigen polymorphism.";
RL EMBO J. 3:1655-1660(1984).
RN [2]
RP SEQUENCE OF 30-266 FROM N.A.
RX MEDLINE=84031733; PubMed=6415003;
RA Larhammar D., Gustafsson G., Andersson M., Bill P., Boelme J.,
RA Claesson L., Denaro M., Emmoth E., Gustafsson K., Hammarling U.,
RA Heidin E., Hyldig-Nielsen J.J., Lind P., Schenning L., Servenius B.,
RA Widmark E., Rask L., Peterson P.A.; II transplantation antigens and
RT "Molecular analysis of human class II transplantation antigens and
RT their genes.";
RL Hum. Immunol. 8:95-103(1983).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00700; CAA25296.1; -.
DR PIR; A02223; HLUH4D.
DR HSSP; P13760; 2SEB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_Cl.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC II; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 266 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 30 123 DR-1 BETA CHAIN.
FT EXTRACELLULAR BETA-1.
```

FT DOMAIN 124 217 EXTRACELLULAR BETA-2.
 FT DOMAIN 218 227 CONNECTING PEPTIDE.
 FT TRANSMEM 228 250
 FT DOMAIN 251 266 CYTOPLASMIC TAIL.
 FT DISULFID 44 108 BY SIMILARITY.
 FT DISULFID 146 202 BY SIMILARITY.
 FT CARBOHYD 48 48 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 266 AA; 30002 MW; 45AB410F8AC21750 CRC64;

Query Match 98.8%; Score 85; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTYCRHNYGV 16
 Db 100 RRAAVDTYCRHNYGV 114

RESULT 2
 HB2D_HUMAN STANDARD; PRT; 266 AA.
 AC P13759;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE HLA class II histocompatibility antigen, DR-1(DW14) beta chain precursor.
 DE HLA-DRB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85296375; PubMed=3875800;
 RX Cairns J.S., Curtsinger J.M., Dahl C.A., Freeman S., Alter B.J.,
 BA Bach F.H.;
 RT "Sequence polymorphism of HLA DR beta 1 alleles relating to T-cell-
 recognized determinants";
 RL Nature 317:166-168(1985).
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X02902; CAA26660.1; -.
 DR PIR; A24431; A24431.
 DR HSP; P13760; 25EB.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR MHC II; Transmembrane; Glycoprotein; Signal.
 KW SIGNAL 1 29
 FT CHAIN 30 266 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
 FT DR-1(DW14) BETA CHAIN.
 FT DOMAIN 30 124
 FT DOMAIN 125 227 EXTRACELLULAR BETA-1.
 FT TRANSMEM 228 250 EXTRACELLULAR BETA-2.
 FT DOMAIN 251 266
 FT DISULFID 44 108 CYTOPLASMIC TAIL.
 FT DISULFID 146 202 BY SIMILARITY.
 FT CARBOHYD 48 48 BY SIMILARITY.
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 266 AA; 30182 MW; AE5C84F1B05DB188 CRC64;

Query Match 98.8%; Score 85; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTYCRHNYGV 16
 Db 100 RRAAVDTYCRHNYGV 114

RESULT 3
 HB2F_HUMAN STANDARD; PRT; 266 AA.
 AC P13758;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE HLA class II histocompatibility antigen, DR-1 beta chain precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86055719; PubMed=2998758;
 RX Tonnelie C., Demars R., Long E.O.;
 RA "DO beta: a new beta chain gene in HLA-D with a distinct regulation
 of expression";
 RL EMBO J. 4:2839-2847(1985).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 32-219.
 RX MEDLINE=94195388; PubMed=8145819;
 RA Stern L.J., Brown J.H., Jardetzky T.J., Gorga J.C., Urban R.G.,
 RA Strominger J.L., Wiley D.C.;
 RA "Crystal structure of the human class II MHC protein HLA-DR1
 complexed with an influenza virus peptide";
 RL Nature 368:215-221(1994).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 32-219.
 RX MEDLINE=93302847; PubMed=8316295;
 RA Brown J.H., Jardetzky T.S., Gorga J.C., Stern L.J., Urban R.G.,
 RA Strominger J.L., Wiley D.C.;
 RA "Three-dimensional structure of the human class II histocompatibility
 antigen HLA-DR1";
 RL Nature 364:33-39(1993).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH SEB.
 RX MEDLINE=94203282; PubMed=8152483;
 RA Jardetzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
 RA Chi Y.I., Stauffacher C., Strominger J.L., Wiley D.C.;
 RA "Three-dimensional structure of a human class II histocompatibility
 molecule complexed with superantigen";
 RL Nature 368:711-718(1994).
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X03069; CAA26873.1; -.
 DR PIR; D24669; D24669.
 DR PDB; 1DLH; 22-JUN-94.
 DR PDB; 1SEB; 20-JUN-96.
 DR PDB; 1AOD; 28-JAN-98.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta; 1.


```
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC II; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 266
FT
FT DOMAIN 30 124
FT DOMAIN 125 227
FT TRANSMEM 228 250
FT DOMAIN 251 266
FT
FT DISULFID 44 108
FT DISULFID 146 202
FT CARBOHYD 48 48
FT SEQUENCE 266 AA; 29914 MW; CC9CC7E2DD0DD036C CRC64;

Query Match 98.8%; Score 85; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
Db 100 RRAAVDTYCRHNYGV 114

RESULT 4
HB2I_HUMAN STANDARD; PRT; 266 AA.
ID HB2I_HUMAN
AC P20039;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class II histocompatibility antigen, DR-5 beta chain precursor.
GN HLA-DRB5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86140021; PubMed=3456344;
RA Tieber V.L., Abruzzini L.F., Didier D.K., Schwartz B.D., Rotwein P.;
RT "Complete characterization and sequence of an HLA class II DR beta
chain cDNA from the DR5 haplotype.";
RL J. Biol. Chem. 261:2738-2742(1986).
CC
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
-----
CC EMBL; M11867; AAA36274.1; -.
CC PIR; A25324; A25324.
CC HSP; P13758; IDLH.
CC MIM; 142857; -.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig-cl.
CC InterPro; IPR000353; MHC_II_beta.
CC Pfam; PF00047; ig; 1.
CC Pfam; PF00969; MHC_II_beta; 1.
CC ProDom; PD000328; MHC_II_beta; 1.
CC SMART; SM00407; IGcl; 1.
CC
-----
CC MHC II; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 266
FT
FT DOMAIN 30 124
FT DOMAIN 125 227
FT
FT HLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
DR-5 BETA CHAIN.
EXTRACELLULAR BETA-1.
EXTRACELLULAR BETA-2.
```

```
FT TRANSMEM 228 250
FT DOMAIN 251 266
FT DISULFID 44 108
FT DISULFID 146 202
FT CARBOHYD 48 48
FT SEQUENCE 266 AA; 30160 MW; 6CFCOD44391B1059 CRC64;

Query Match 98.8%; Score 85; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
Db 100 RRAAVDTYCRHNYGV 114

RESULT 5
HB2H_HUMAN STANDARD; PRT; 266 AA.
ID HB2H_HUMAN
AC P13760;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class II histocompatibility antigen, DR-4 beta chain precursor
(DRB1*0401).
GN HLA-DRB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87250499; PubMed=3036826;
RA Andersson G., Larhammar D., Widmark E., Serenius B., Peterson P.A.,
RA Rask L.;
RT "Class II genes of the human major histocompatibility complex.
Organization and evolutionary relationship of the DR beta genes.";
RL J. Biol. Chem. 262:8748-8758(1987).
RN [2]
RP REVISIONS.
RA Andersson G., Larhammar D., Widmark E., Serenius B., Peterson P.A.,
RA Rask L.;
RL J. Biol. Chem. 263:8551-8551(1988).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH COLLAGEN.
RX MEDLINE=98014591; PubMed=9354468;
RA Dessen A., Lawrence C.M., Cupo S., Zaller D.M., Wiley D.C.;
RT "X-ray crystal structure of HLA-DR4 (DRA*0101, DRB1*0401) complexed
with a peptide from human collagen II.";
RL Immunity 7:473-481(1997).
CC
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
-----
CC EMBL; M20548; -. NOT_ANNOTATED_CDS.
CC EMBL; M20549; -. NOT_ANNOTATED_CDS.
CC EMBL; M20550; -. NOT_ANNOTATED_CDS.
CC PIR; A29310; A29310.
CC PDB; 2SEB; 28-JAN-98.
CC MIM; 142857; -.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig-cl.
CC InterPro; IPR000353; MHC_II_beta.
CC Pfam; PF00047; ig; 1.
CC Pfam; PF00969; MHC_II_beta; 1.
CC ProDom; PD000328; MHC_II_beta; 1.
CC SMART; SM00407; IGcl; 1.
```

DR	PROSITE; PS00290; IG_MHC; 1.
MHC II; transmembrane; Glycoprotein; Signal; 3D-structure.	
FT SIGNAL	1 29
FT CHAIN	30 266
FT FT	
FT DOMAIN	30 124
FT DOMAIN	125 227
FT TRANSMEM	228 250
FT DOMAIN	251 266
FT DISULFID	44 108
FT DISULFID	146 202
FT CARBOHYD	48
FT SEQUENCE	266 AA; 30112 MW; 8116E91DA38294E5 CRC64;
Query Match	95.3%; Score 82; DB 1; Length 266;
Best Local Similarity	93.3%; Pred. No. 6.8e-07;
Matches 14; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
Qy	2 RRAAVDTYCRHNYGV 16
	:
Db	100 KRAAVDTYCRHNYGV 114
RESULT	6
HB2G_HUMAN	
ID ID	HB2G_HUMAN STANDARD; PRT; 198 AA.
AC AC	P01911;
DT DT	21-JUL-1986 (Rel. 01, Created)
DT DT	21-JUL-1986 (Rel. 01, Last sequence update)
DE DE	16-OCT-2001 (Rel. 40, Last annotation update)
DE DE	HLA class II histocompatibility antigen, DW2.2/DR2.2 beta chain (Fragment).
OS OS	Homo sapiens (Human).
OC OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NBBI_Taxid=9606;	
RN RN	[1]
RP RP	SEQUENCE.
RX RX	MEDLINE=62096757; PubMed=6247956;
RA RA	Kratzin H., Yang C.-Y., Gotz H., Pauly E., Kolbel S., Egert G.,
RA RA	Thinnes F.P., Wernet P., Altevoigt P., Hilschmann N.;
RT RT	"Primary structure of class II human histocompatibility antigens. 1st communication. Amino acid sequence of the N-terminal 198 residues of the beta chain of a HLA-Dw2.2; DR2.2-alloantigen.";
RL RL	Hoppe-Seyler's Z. Physiol. Chem. 362:1669-1669(1981).
CC CC	-I- MISCELLANEOUS: THE CHAIN SHOWN CONSTITUTED ABOUT 70% OF A POOL OF AT LEAST SEVEN SIMILAR BETA CHAINS.
CC CC	PIR; A02220; HLHWB.
DR DR	HSSP; P13758; IDLH.
DR DR	InterPro; IPR003006; Ig_MHC.
DR DR	InterPro; IPR003597; Ig_cl
DR DR	InterPro; IPR000353; MHC_II_beta.
DR DR	Pfam; PF00047; Ig; 1.
DR DR	Pfam; PF00969; MHC_II_beta; 1.
DR DR	ProDom; PD000328; MHC_II_beta; 1.
DR DR	SMART; SM00407; IGcl; 1.
DR DR	PROSITE; PS00290; IG_MHC; 1.
KW KW	MHC II; Transmembrane; Glycoprotein.
FT FT	DOMAIN 1 94
FT FT	DOMAIN 95 187
FT FT	DOMAIN 188 197
FT FT	TRANSMEM 198 >198
FT FT	DISULFID 15 79
FT FT	DISULFID 117 172
FT FT	CARBOHYD 19 19
FT FT	NON_TER 198 198
FT FT	SEQUENCE 198 AA; 22965 MW; 18199D91A4D737EC CRC64;
Query Match	93.0%; Score 80; DB 1; Length 198;
Best Local Similarity	100.0%; Pred. No. 1.1e-06;
Matches ~14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

EMBL; M16942; AAA36296.1; -
 PIR; B28031; B28031.
 HSP; P13760; 2SER.
 InterPro; IPR003006; Ig_MHC.
 InterPro; IPR003597; Ig_C1.
 InterPro; IPR003533; MHC_II_beta.
 Pfam; PF00047; Ig_1.
 Pfam; PF00969; MHC_II_beta; 1.
 ProDom; PD000328; MHC_II_beta; 1.
 SMART; SM00407; IG_C1; 1.
 PROSITE; PS00290; IG_MHC; 1.
 MHC II; Transmembrane; Glycoprotein; Signal.
 SIGNAL 1 29
 CHAIN 30 266 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-W53 BETA CHAIN.
 DOMAIN 30 124 EXTRACELLULAR BETA-1.
 DOMAIN 125 227 EXTRACELLULAR BETA-2.
 TRANSMEM 228 250
 DOMAIN 251 266
 DISULFID 44 108 CYTOPLASMIC TAIL.
 DISULFID 146 202 BY SIMILARITY.
 CARBOHYD 48 48 BY SIMILARITY.
 SEQUENCE 266 AA; 29971 MW; 32AE1AF1334423AF CRC64;

Query Match 86.0%; Score 74; DB 1; Length 266;
 Best Local Similarity 86.7%; Pred. No. 1.6e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
 III IIIIIIIIIII
 DB 100 RRAEVDTYCRHNYGV 114

RESULT 10
 HB24_MOUSE STANDARD; PRT; 264 AA.
 ID AC P20040;
 IC 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DE H-2 class II histocompatibility antigen, E-Q beta chain precursor (E-W17).
 DE OS Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=89035495; PubMed=2460545;
 RX Vu T.H., Tacchini-Cottier F.M., Day C.E., Begovich A.B., Jones P.P.;
 RT "Molecular basis for the defective expression of the mouse Ew17 beta gene";
 RT J. Immunol. 141:3654-3661(1988).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=90171595; PubMed=2106558;
 RX Begovich A.B., Vu T.H., Jones P.P.;
 RT "Characterization of the molecular defects in the mouse E beta f and E beta g genes. Implications for the origin of MHC polymorphism.";
 RT J. Immunol. 144:1957-1964(1990).
 RL
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; M23693; -; NOT_ANNOTATED_CDS.
 DR EMBL; M35682; AAA39595.1; -
 DR EMBL; M35680; AAA39595.1; JOINED.
 DR EMBL; M35681; AAA39595.1; JOINED.
 DR PUR; A30529; A30529.
 DR HSP; P13760; 2SEB.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IG1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 MHC II; Transmembrane; Glycoprotein; Signal.
 KW MHC II; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 264 H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN,
 FT E-Q BETA CHAIN.
 FT DOMAIN 27 121 EXTRACELLULAR BETA-1.
 FT DOMAIN 122 225 EXTRACELLULAR BETA-2.
 FT TRANSMEM 226 246 POTENTIAL.
 FT DOMAIN 247 264 CYTOPLASMIC TAIL.
 FT DISULFID 38 106 BY SIMILARITY.
 FT DISULFID 144 200 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 264 AA; 30204 MW; FF81C532A9B72D7A CRC64;

Query Match 84.9%; Score 73; DB 1; Length 264;
 Best Local Similarity 80.0%; Pred. No. 2.3e-05;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRAVDYTCRHNYGV 16
 :|||||
 Db 98 KRAVDYTCRHNYEI 112

RESULT 11
 HB2I_MOUSE
 ID HB2I_MOUSE STANDARD; PRT; 264 AA.
 AC P18458;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE H-2 class II histocompatibility antigen, I-A beta chain precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NONOBSE DIABETIC / NOD; TISSUE-Spleen;
 RX MEDLINE=91310089; PubMed=1855817;
 RA Acha-Orbea H., Scarpellino L.;
 RT "Nonobese diabetic and nonobese nondiabetic mice have unique MHC
 class II haplotypes";
 RL Immunogenetics 34:57-59(1991).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; X52641; CAA36863.1; -

DR HSP; P13760; 2SEB.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IG1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 MHC II; Transmembrane; Glycoprotein; Signal.
 KW MHC II; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 31
 FT CHAIN 32 264 H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN,
 FT I-A BETA CHAIN.
 FT DOMAIN 32 121 EXTRACELLULAR BETA-1.
 FT DOMAIN 122 215 EXTRACELLULAR BETA-2.
 FT TRANSMEM 216 225 CONNECTING PEPTIDE.
 FT DOMAIN 226 248
 FT DOMAIN 249 264 CYTOPLASMIC TAIL.
 FT DISULFID 42 106 BY SIMILARITY.
 FT DISULFID 144 200 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 264 AA; 30231 MW; 04529F5E527D7A CRC64;

Query Match 84.9%; Score 73; DB 1; Length 264;
 Best Local Similarity 80.0%; Pred. No. 2.3e-05;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRAVDYTCRHNYGV 16
 :|||||
 Db 98 KRAVDYTCRHNYEI 112

RESULT 12
 HB22_MOUSE
 ID HB22_MOUSE STANDARD; PRT; 264 AA.
 AC P01915;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE H-2 class II histocompatibility antigen, E-D beta chain precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=83300003; PubMed=6310581;
 RA Saito H., Maki R.A., Clayton L.K., Tonegawa S.;
 RT "Complete primary structures of the E beta chain and gene of the
 mouse major histocompatibility complex";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:5520-5524(1983).
 RN [2]
 RP SEQUENCE OF 1-31 FROM N.A.
 RX MEDLINE=84270753; PubMed=6087163;
 RA Gillies S.D., Folsom V., Tonegawa S.;
 RT "Cell type-specific enhancer element associated with a mouse MHC
 gene, E beta";
 RL Nature 310:594-597(1984).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

or send an email to license@isb-sib.ch.

```

CC EMBL; X00777; CAA25354.1; -.
CC EMBL; K00123; -. NOT_ANNOTATED_CDS.
CC PIR; A02225; HLMSEB.
CC HSSP; P13760; 2SEB.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_cl.
CC InterPro; IPR000353; MHC_II_beta.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00969; MHC_II_beta; 1.
CC ProDom; PD000328; MHC_II_beta; 1.
CC SMART; SM00407; IGcl; 1.
CC PROSITE; PS00290; IG_MHC; 1.
CC MHC II; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 31
FT CHAIN 32 264
FT DOMAIN 32 121
FT DOMAIN 122 215
FT DOMAIN 216 225
FT TRANSMEM 226 248
FT DOMAIN 249 264
FT DISULFID 42 106
FT DISULFID 144 200
FT CARBOHYD 46 46
FT SEQUENCE 264 AA; 30049 MW; 29117F30B8A56942 CRC64;

```

Query Match 79.1%; Score 68; DB 1; Length 264;

Best Local Similarity 78.6%; Pred. No. 0.00017;

Matches 11; Conservative 2; Mismatches 1; Indels. 0; Gaps 0;

Qy 3 RAAVDTCYCRHNYGV 16

||:|||||||

Db 99 RASVDTCYCRHNYEI 112

RESULT 13

```

ID HB2A_HUMAN STANDARD; PRT; 266 AA.
AC P01913;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class II histocompatibility antigen, DR-1 beta chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Long E.O., Wake C.T., Gorski J., Mach B.;
RT "Complete sequence of an HLA-DR beta chain deduced from a cDNA clone
RT and identification of multiple non-allelic DR beta chain genes.";
RL EMO J. 2:389-394(1983).
RN [2]
RP SEQUENCE OF 30-266 FROM N.A. (DR4/WB B-CELL LINE).
RX MEDLINE=84031722; PubMed=6414998;
RA Long E.O., Gorski J., Rollini P., Wake C.T., Strubin M.,
RA Rabourdin-Combe C., Mach B.;
RT "Molecular analysis of the genes for human class II antigens of the
RT major histocompatibility complex.";
RL Hum. Immunol. 8:113-121(1983).

```

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

```

DR EMBL; V00522; CAA23781.1; -.
DR EMBL; A06800; CAA00596.1; -.
DR PIR; A02222; HLHU5D.
DR HSSP; P13760; 2SEB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR MHC II; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 266
FT DOMAIN 30 124
FT DOMAIN 125 227
FT TRANSMEM 228 250
FT DOMAIN 251 266
FT TRANSMEM 251 266
FT DISULFID 44 108
FT DISULFID 146 202
FT CARBOHYD 48 48
FT SEQUENCE 266 AA; 30031 MW; BB3BF977FDC95947 CRC64;

```

Query Match 79.1%; Score 68; DB 1; Length 266;

Best Local Similarity 73.3%; Pred. No. 0.00017;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RRAVDTCYCRHNYGV 16

:|:|||||||

Db 100 KRQVDYCRHNYGV 114

RESULT 14

```

ID HB2B_HUMAN STANDARD; PRT; 266 AA.
AC P01912;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class II histocompatibility antigen, DR-1 beta chain precursor
DE (Clone P2-beta-3).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84261468; PubMed=6589154;
RA Peterson P.A., Gustafsson K., Wiman K.G., Emmoth E., Larhammar D.,
RA Boehme J., Hyldig-Nielsen J.J., Ronne H., Rask L.;
RT "Mutations and selection in the generation of class II
RT histocompatibility antigen polymorphism.";
RL EMO J. 3:1655-1660(1984).
RN [2]
RP SEQUENCE OF 30-266 FROM N.A.
RX MEDLINE=84031733; PubMed=6415003;
RA Larhammar D., Andersson G., Andersson M., Bill P., Boehme J.,
RA Claesson L., Denaro M., Emmoth E., Gustafsson K., Hammarling U.,
RA Heidlin E., Hyldig-Nielsen J.J., Lind P., Schenning L., Servenius B.,
RA Widmark E., Rask L., Peterson P.A.;
RT "Molecular analysis of human class II transplantation antigens and
RT their genes.";
RL Hum. Immunol. 8:95-103(1983).

```

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

or send an email to license@isb-sib.ch.

```
CC -----
CC EMBL; X00699; CAA25295.1; -
CC PIR; A02221; HLHU3D.
CC HSP; P13758; IDLH.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR InterPro; IPR003597; Ig_cl.
CC DR InterPro; IPR00353; MHC_II_beta.
CC DR Pfam; PF00047; Ig; 1.
CC DR Pfam; PF00969; MHC_II_beta; 1.
CC DR ProDom; PD000328; MHC_II_beta; 1.
CC DR SMART; SM00407; IGC1; 1.
CC DR PROSITE; PS00290; IG_MHC; 1.
CC DR MHC II; Transmembrane; Glycoprotein; Signal.
CC FT SIGNAL 1 29
CC FT CHAIN 30 266
CC FT HLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
CC FT DR-1 BETA CHAIN.
CC FT DOMAIN 30 123
CC FT EXTRACELLULAR BETA-1.
CC FT DOMAIN 124 217
CC FT EXTRACELLULAR BETA-2.
CC FT DOMAIN 218 227
CC FT CONNECTING PEPTIDE.
CC FT TRANSMEM 228 250
CC FT DOMAIN 251 266
CC FT CYTOPLASMIC TAIL.
CC FT DISULFID 44 108
CC FT BY SIMILARITY.
CC FT DISULFID 146 202
CC FT BY SIMILARITY.
CC FT CARBOHYD 48 48
CC FT N-LINKED (GLCNAC... ) (POTENTIAL).
CC SQ SEQUENCE 266 AA; 30120 MW; 37329B097C6BEEB4 CRC64;

Query Match 79.1%; Score 68; DB 1; Length 266;
Best Local Similarity 73.3%; Pred. No. 0.00017;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
DB 100 KRQVDNYCRHNYGV 114

RESULT 15
HB2E_HUMAN
ID HB2E_HUMAN STANDARD; PRT; 266 AA.
AC P04229;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class II histocompatibility antigen, DR-1 beta chain precursor
DE (Clone 2918.4).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85216509; PubMed=3858829;
RA Bell J.I., Estess P., St John T., Saiki R., Watling D.L.,
RA Erlich H.A., McDewitt H.O.;
RT "DNA sequence and characterization of human class II major
RT histocompatibility complex beta chains from the DR1 haplotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3405-3409(1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M11161; AAA59781.1; -
CC PIR; A02224; HLHU1B.
CC HSP; P13758; IDLH.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR InterPro; IPR003597; Ig_cl.
CC DR InterPro; IPR00353; MHC_II_beta.
```

```
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR MHC II; Transmembrane; Glycoprotein; Signal.
DR FT SIGNAL 1 29
DR FT CHAIN 30 266
DR FT HLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
DR FT DR-1 BETA CHAIN.
DR FT DOMAIN 30 124
DR FT EXTRACELLULAR BETA-1.
DR FT DOMAIN 125 227
DR FT EXTRACELLULAR BETA-2.
DR FT TRANSMEM 228 250
DR FT DOMAIN 251 266
DR FT CYTOPLASMIC TAIL.
DR FT DISULFID 44 108
DR FT BY SIMILARITY.
DR FT DISULFID 146 202
DR FT BY SIMILARITY.
DR FT CARBOHYD 48 48
DR FT N-LINKED (GLCNAC... ) (POTENTIAL).
DR SQ SEQUENCE 266 AA; 30041 MW; EC56FB912D4E386F CRC64;
```

Query Match 79.1%; Score 68; DB 1; Length 266;
Best Local Similarity 73.3%; Pred. No. 0.00017;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
DB 100 KRQVDNYCRHNYGV 114

Search completed: July 1, 2002, 12:23:53
Job time: 200 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 12:20:13 ; Search time 25.25 Seconds
(without alignments)
109.621 Million cell updates/sec

Title: US-09-832-510-2
Perfect score: 86
Sequence: 1 XRRRAVDTCRHNHYGV 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Description
1	85	98.8	P79469 cervus elap
2	85	98.8	P79470 cervus elap
3	85	98.8	Q30009 homo sapien
4	85	98.8	Q29834 homo sapien
5	85	98.8	Q9my12 homo sapien
6	85	98.8	Q9my11 homo sapien
7	85	98.8	Q9my08 homo sapien
8	85	98.8	Q9my07 homo sapien
9	85	98.8	Q9mxz5 homo sapien
10	85	98.8	Q9mxz2 homo sapien
11	85	98.8	Q9mxz1 homo sapien
12	85	98.8	Q30128 homo sapien
13	85	98.8	Q30156 homo sapien
14	85	98.8	Q29646 homo sapien
15	85	98.8	Q9my02 homo sapien
16	85	98.8	Q9my02 homo sapien

17	85	98.8	74	7	Q9MY01	Q9my01 homo sapien
18	85	98.8	74	7	Q9MY00	Q9my00 homo sapien
19	85	98.8	74	7	Q9MX28	Q9mx28 homo sapien
20	85	98.8	74	7	Q9MX27	Q9mx27 homo sapien
21	85	98.8	74	7	Q29903	Q29903 homo sapien
22	85	98.8	74	7	Q29727	Q29727 homo sapien
23	85	98.8	75	6	Q9GM64	Q9gm64 bos taurus
24	85	98.8	75	6	Q9TTL3	Q9ttl3 bos taurus
25	85	98.8	75	7	Q9GJB7	Q9gjb7 bos taurus
26	85	98.8	75	7	Q29802	Q29802 homo sapien
27	85	98.8	78	7	Q98047	Q98047 homo sapien
28	85	98.8	78	7	Q29906	Q29906 homo sapien
29	85	98.8	78	7	Q29735	Q29735 homo sapien
30	85	98.8	78	7	Q29736	Q29736 homo sapien
31	85	98.8	78	7	Q95IY3	Q95iy3 bos indicus
32	85	98.8	79	7	Q9GIX7	Q9gix7 homo sapien
33	85	98.8	79	7	Q29691	Q29691 homo sapien
34	85	98.8	80	7	Q02951	Q02951 homo sapien
35	85	98.8	80	7	Q19667	Q19667 homo sapien
36	85	98.8	80	7	Q29806	Q29806 homo sapien
37	85	98.8	80	7	Q02969	Q02969 homo sapien
38	85	98.8	81	7	Q30753	Q30753 macaca neme
39	85	98.8	81	7	Q95382	Q95382 homo sapien
40	85	98.8	81	7	Q99948	Q99948 homo sapien
41	85	98.8	81	7	P79486	P79486 homo sapien
42	85	98.8	81	7	O00283	O00283 homo sapien
43	85	98.8	81	7	O46700	O46700 homo sapien
44	85	98.8	82	7	O78108	O78108 homo sapien
45	85	98.8	82	7	Q30258	Q30258 bos taurus

ALIGNMENTS

RESULT 1

P79469 ID P79469 PRELIMINARY; PRT; 39 AA.
AC P79469;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63072; AAB37772.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4752 MW; 0D621B08AD0ECF58 CRC64;

Query Match 98.8%; Score 85; DB 7; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTCRHNHYGV 16

Db 16 RRAAVDTCRHNHYGV 30

RESULT 2

P79470

```
ID P79470 PRELIMINARY; PRT; 39 AA.
AC P79470;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RT "The MHC class II DRB intron 2 microsatellite of red deer.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63073; AAB37773.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 39
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4693 MW; 27481B08AD0ECC0E CRC64;

Query Match 98.8%; Score 85; DB 7; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYG 16
Db 16 RRAAVDTYCRHNYG 30
|||||

RESULT 3
Q30009 PRELIMINARY; PRT; 50 AA.
AC Q30009;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HLA-DRB1 PROTEIN (FRAGMENT).
GN HLA-DRB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87090380; PubMed=3099214;
RA Wu S., Saunders T.L., Bach F.H.;
RT "Polymorphism of human Ia antigens generated by reciprocal intergenic
exchange between two DR beta loci.";
RL Nature 324:676-679(1986).
DR EMBL; M30182; AAA59715.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 50
FT NON_TER 50 50
SQ SEQUENCE 50 AA; 5913 MW; 479629A86A3250BF CRC64;

Query Match 98.8%; Score 85; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYG 16
Db 27 RRAAVDTYCRHNYG 41
|||||
```

```
RESULT 4
Q29834 PRELIMINARY; PRT; 72 AA.
ID Q29834;
AC Q29834;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HLA-DRB1*1605 PROTEIN (FRAGMENT).
GN HLA-DRB1*1605.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94164706; PubMed=8119741;
RA Bettinotti M.P., McNicholas A., Keller E., Andreas A., Scholz S.,
RT Albert E.D.;
RT "DRB1*1605: a new DR2-DRB1 allele found in a German family.";
RL Immunogenetics 39:300-300(1994).
DR EMBL; X74343; CAA52390.1; -.
DR HSSP; P13758; IAQD.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 72
FT NON_TER 72 72
SQ SEQUENCE 72 AA; 8634 MW; 8B25AF1AE63C5312 CRC64;
```

```
Query Match 98.8%; Score 85; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 RRAAVDTYCRHNYG 16
Db 57 RRAAVDTYCRHNYG 71
|||||
```

```
RESULT 5
Q9MY12 PRELIMINARY; PRT; 73 AA.
ID Q9MY12;
AC Q9MY12;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC CLASS II ANTIGEN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=BLLOOD;
RA Arnaiz-Villena A.;
RT "HLA class II polymorphism.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029270; AAF65480.1; -.
DR HSSP; P13758; IAQD.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 73
FT NON_TER 73 73
SQ SEQUENCE 73 AA; 8918 MW; 89DB524AFF9C5C9 CRC64;
```

```
Query Match 98.8%; Score 85; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


Query Match 98.8%; Score 85; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTCRHNYGV 16
|||||
DB 58 RRAAVDTCRHNYGV 72

RESULT 10
Q9MXZ2 PRELIMINARY; PRT; 73 AA.
AC Q9MXZ2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC CLASS II ANTIGEN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Arnal-Villena A.;
RT "HLA class II polymorphism";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029291; AAF65500.1; -;
DR HSSP; P13758; IAQD.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 73
SQ SEQUENCE 73 AA; 8797 MW; DE61BE4479FD5312 CRC64;

Query Match 98.8%; Score 85; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTCRHNYGV 16
|||||
DB 58 RRAAVDTCRHNYGV 72

RESULT 11
Q9MXZ1 PRELIMINARY; PRT; 73 AA.
AC Q9MXZ1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC CLASS II ANTIGEN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Arnal-Villena A.;
RT "HLA class II polymorphism";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029292; AAF65501.1; -;
DR HSSP; P13758; IAQD.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.

FT NON_TER 1
FT NON_TER 73
SQ SEQUENCE 73 AA; 8763 MW; DE61BE49149D5312 CRC64;

Query Match 98.8%; Score 85; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTCRHNYGV 16
|||||
DB 58 RRAAVDTCRHNYGV 72

RESULT 12
Q30128 PRELIMINARY; PRT; 73 AA.
AC Q30128;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HLA-DRB1 PROTEIN (FRAGMENT).
GN HLA-DRB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Lester S., Cassidy S., McCluskey J.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; L27216; AAA59789.1; -;
DR HSSP; P13758; IAQD.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 73
SQ SEQUENCE 73 AA; 8812 MW; DE6C0522195B2275 CRC64;

Query Match 98.8%; Score 85; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTCRHNYGV 16
|||||
DB 58 RRAAVDTCRHNYGV 72

RESULT 13
Q30156 PRELIMINARY; PRT; 73 AA.
AC Q30156;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC CLASS II HLA-DR4/DW14 (FRAGMENT).
GN HLA-DRB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9116981; PubMed-2003917;
RA Kaneoka H., Lee D.R., Hsu K.C., Sharp G.C., Hoffman R.W.;
RT "Solid-phase direct DNA sequencing of allele-specific polymerase chain
RT reaction-amplified HLA-DR genes";
RL Biotechniques 10:30-30(1991).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=92118143; PubMed=1370621;
RA Kaneoka H., Hsu K.C., Takeda Y., Sharp G.C., Hoffman R.W.;
RT "Molecular genetic analysis of HLA-DR and HLA-DQ genes among anti-U1-
70-kD autoantibody positive connective tissue disease patients.";
RL Arthritis Rheum. 35:83-94(1992).
DR EMBL; M63338; AAC41709.1; -;
DR HSP; P13758; IAQD.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 73 AA; 8876 MW; D3862FA471EB8C5 CRC64;

Query Match 98.8%; Score 85; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDYCRHNYGV 16
Db 57 RRAAVDYCRHNYGV 71
|||||

RESULT 14

Q29646 PRELIMINARY; PRT; 73 AA.
AC Q29646;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC CLASS II HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
GN HLA-DRB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=96232970; PubMed=8655358;
RA Dinanuer D.M., Glumm R., Baxter-Lowe L.A.;
RT "DRB1*1316: evolutionary and functional implications of a novel
polymorphism at codon 86";
RL Hum. Immunol. 45:37-41(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Baxter-Lowe L.A.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U08274; AAB87709.1; -;
DR HSP; P13758; IAQD.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
FT NON_TER 73 73
SQ SEQUENCE 73 AA; 8858 MW; 26CE9629C29D5301 CRC64;

Query Match 98.8%; Score 85; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDYCRHNYGV 16
Db 58 RRAAVDYCRHNYGV 72
|||||

RESULT 15

Q9UEX9

ID Q9UEX9 PRELIMINARY; PRT; 74 AA.
AC Q9UEX9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HUMAN LEUCOCYTE ANTIGEN B (FRAGMENT).
GN HLA-DRB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD MONONUCLEAR CELLS;
RA Beer U., Schmidrathner K., Gleissner B., Fae I., Fischer G.F.;
RT "A new HLA-DRB1*11 allele found in an Austrian bone marrow donor";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ252281; CAB65734.1; -;
DR HSP; P13758; IAQD.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
FT NON_TER 74 74
SQ SEQUENCE 74 AA; 9019 MW; DE2A9CF68044C812 CRC64;

Query Match 98.8%; Score 85; DB 7; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDYCRHNYGV 16
Db 59 RRAAVDYCRHNYGV 73
|||||

Search completed: July 1, 2002, 12:23:36
Job time: 203 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 12:16:23 ; Search time 30.04 Seconds
(without alignments)
59.160 Million cell updates/sec

Title: US-09-832-510-2

Perfect score: 86

Sequence: 1 XRRAAVDTYCRHNGV 16

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	98.8	16	AA01978	Lym-1 antibody-rea
2	85	98.8	25	AA04934	DRI beta chain pos
3	85	98.8	25	AA041656	Immunomodulatory p
4	85	98.8	89	AA024276	DRI. Synthetic.
5	85	98.8	89	AA14343	Protein encoded by
6	85	98.8	89	AA14344	Protein encoded by
7	85	98.8	89	AA14336	Protein encoded by
8	85	98.8	89	AA14337	Protein encoded by
9	85	98.8	89	AA14341	Protein encoded by
10	85	98.8	89	AA14342	Protein encoded by
11	85	98.8	89	AA14329	Protein encoded by

12	85	98.8	89	17	AA14332	Protein encoded by
13	85	98.8	89	17	AA14310	Protein encoded by
14	85	98.8	89	17	AA14314	Protein encoded by
15	85	98.8	89	17	AA14319	Protein encoded by
16	85	98.8	89	22	AA071746	Protein encoded by
17	85	98.8	89	22	AA07831	Protein encoded by
18	85	98.8	89	22	AA07843	Protein encoded by
19	85	98.8	89	22	AA07847	Protein encoded by
20	85	98.8	89	22	AA07853	Protein encoded by
21	85	98.8	89	22	AA07854	Protein encoded by
22	85	98.8	89	22	AA07857	Protein encoded by
23	85	98.8	89	22	AA07862	Protein encoded by
24	85	98.8	89	22	AA07863	Protein encoded by
25	85	98.8	89	22	AA07864	Protein encoded by
26	85	98.8	89	22	AA07867	Protein encoded by
27	85	98.8	89	22	AA07875	Protein encoded by
28	85	98.8	89	22	AA07876	Protein encoded by
29	85	98.8	102	22	AA069574	Human HLA-DR B1 an
30	85	98.8	124	22	AA080794	Human haematologic
31	85	98.8	124	22	AA081238	Human haematologic
32	85	98.8	124	22	AA081844	Human haematologic
33	85	98.8	174	20	AA06802	Peptide Seq ID No:
34	85	98.8	177	22	AA080429	Human haematologic
35	85	98.8	177	22	AA081066	Human haematologic
36	85	98.8	177	22	AA081769	Human haematologic
37	85	98.8	237	16	AA074038	MHC polypeptide HL
38	85	98.8	266	21	AA068283	Class II beta chai
39	85	98.8	266	21	AA052937	Class II beta chai
40	85	98.8	266	22	AA014510	Human novel protei
41	85	98.8	266	22	AA058698	Class II beta chai
42	85	98.8	308	22	AA030921	Novel human secret
43	82	95.3	34	22	AA069573	Chimeric peptide t
44	82	95.3	80	20	AA055741	HLA allele DRB1*04
45	82	95.3	84	10	AA090034	Peptide of human/m

ALIGNMENTS

RESULT¹

AA01978

ID AA01978 standard; peptide; 16 AA.

XX

AC AA01978;

XX

DT 25-SEP-2000 (first entry)

XX

DE Lym-1 antibody-reactive HLA-DR epitope #3.

XX

KW Lym-1 antibody reactive epitope: HLA-DR; MHC Class II;

KW major histocompatibility complex; non-Hodgkin's B cell lymphoma;

KW B-NHL cell; immunogenic; vaccine; therapy; cancer.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 1 /label= Gln, Lys, Arg

XX

PN WO200024777-A1.

XX

PD 04-MAY-2000.

XX

PF 12-OCT-1999; 99WO-US23609.

XX

PR 28-OCT-1998; 98US-0181896.

XX

PA (RECC) UNIV CALIFORNIA.

XX

PI Rose LM, Meares CF, O'Donnell RT;

XX

DR WPI; 2000-365109/31.

XX

PT Novel peptide epitopes recognized by the non-Hodgkin's B-cell lymphoma
PT Lym-1 antibody, useful for generating antibodies for treating
PT non-Hodgkin's B-cell lymphoma -
XX
XX
XX Claim 3; Page 30; 39pp; English.
XX
XX The invention relates to a novel immunogenic composition comprising an
CC isolated or recombinant peptide epitope derived from HLA-DR, a human
CC Class II major histocompatibility (MHC) molecule. The peptide is 16 amino
CC acids long and is capable of generating an immune response to a non-
CC Hodgkin's B cell lymphoma (B-NHL) cell, as determined by its reactivity
CC with the Lym-1 monoclonal antibody. The Lym-1 antibody selectively binds
CC an antigen, typically a variant form of the HLA-DR molecule, which is
CC highly expressed on the surface of most B-NHL lymphomas. The Lym-1
CC antigen is found only at low levels in normal cells. The HLA-DR Lym-1
CC reactive peptide is of the general formula
CC X1-A9g-X2-X3-X4-X5-X6-Thr-X7-X8-X9-X10-X11-X12-X13-Val, where:
CC X1 is Gln, Lys or Arg;
CC X2 and X3 are independently any amino acid;
CC X4 is Ala, Gln, Asp, Val, Leu or Ile;
CC X5 and X6 are independently any amino acid; and
CC X7, X8, X9, X10, X11, X12, X13 are independently any amino acid.
CC The peptides of the invention can be administered to a cancer patient in
CC order to generate antibodies reactive with a B-NHL cell. They can also be
CC used to raise antibodies in other animals. The peptides, and nucleotides
CC encoding them can be used to identify patients who will be responsive to
CC a Lym-1 antibody used as a cytotoxic therapeutic agent. The present
CC sequence represents a specific embodiment of a Lym-1 reactive epitope of
CC the invention.
XX
XX
SQ Sequence 16 AA;

Query Match 98.8%; Score 85; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
| | | | | | | | | | | | | | | |
Db 2 rraavdtcychrnygv 16

RESULT 2
AAR49334
ID AAR49334 standard; Protein; 25 AA.
XX
XX AAR49334;
XX
XX 16-SEP-1994 (first entry)
XX
XX DR1 beta chain position 66-90.
XX
XX Naturally-occurring; immunomodulatory protein; human; therapy; class I;
KW major histocompatibility complex; class II; allotype; type I diabetes;
KW autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
KW multiple sclerosis; transplant rejection; vaccine; MHC.
XX
XX Homo sapiens.
XX
XX W09404171-A.
XX
XX 03-MAR-1994.
XX
XX 11-AUG-1993; 93WO-0507545.
XX
XX 11-AUG-1992; 92US-0925460.
XX
XX 15-JUN-1993; 93US-0925460.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Chicz RM, Hedley ML, Stern LJ, Strominger JL, Urban RG;
PI Vignall DA;
XX

DR WPI; 1994-082825/10.
XX
XX Novel immunomodulatory peptide(s) and nucleic acids - useful for
PT treatment of autoimmune diseases, transplant rejection and for
PT vaccination
XX
XX Disclosure; Page 38; 139pp; English.
XX
XX The sequences given in AAR49291-505 and AAR45981-7038 represent peptide
CC fragments of naturally-occurring immunomodulatory proteins. These
CC fragments are between 10-30 residues in length and bind to a human
CC major histocompatibility complex (MHC) class II allotype. These
CC peptides may be used for therapy of autoimmune diseases, such as
CC type I diabetes, rheumatoid arthritis and multiple sclerosis, and to
CC reduce transplant rejection. They may also be used for vaccination
CC providing an exclusively T-cell-mediated response, which can be
CC class I or class-II based, or both, depending on the length and
CC character of the immunogenic peptides.
XX
XX Sequence 25 AA;

Query Match 98.8%; Score 85; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
| | | | | | | | | | | | | | | |
Db 6 rraavdtcychrnygv 20

RESULT 3
AAW41656
ID AAW41656 standard; peptide; 25 AA.
XX
XX AAW41656;
XX
XX 27-APR-1998 (first entry)
XX
XX Immunomodulatory peptide.
XX
XX Immunomodulator; immunosuppressant; immunostimulant; treatment;
KW transplant rejection; autoimmune disease; cancer; infection.
XX
XX Synthetic.
XX
XX W09739023-A1.
XX
XX 23-OCT-1997.
XX
XX 04-APR-1997; 97WO-SE00574.
XX
XX 23-SEP-1996; 96SE-0003469.
XX
XX 12-APR-1996; 96SE-0001422.
XX
XX (ASTR) ASTRA AB.
XX
XX Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;
XX
XX WPI; 1997-526397/48.
XX

XX Nucleic acids encoding cysteine- or methionine-containing peptide(s)
PT which have immunostimulatory or immunosuppressive activity - can be
PT used to treat, e.g. cancers, infection, autoimmune disease or
PT transplant rejection
XX
XX Claim 1; Page 18; 183pp; English.
XX
XX A novel immunosuppressing or immunostimulatory peptide conforms to
CC the motifs represented by the formulae of the invention, with the
CC proviso that the peptides described in AAW36999, AAW37000 and AAW41647
CC to AAW41682 are excluded.
CC An immunosuppressant can be used to treat transplant rejection or

CC autoimmune disease, e.g. rheumatoid arthritis, systemic lupus
 CC erythematosis, Sjogren's syndrome, scleroderma, mixed connective
 CC tissue disease, dermatomyositis, polymyositis, Reiter's syndrome,
 CC Behcet's disease, type I diabetes, Hashimoto's thyroiditis, Graves'
 CC disease, multiple sclerosis, myasthenia gravis, encephalomyelitis,
 CC pheniphagus vulgaris, vegetans or foliaceus, Seneear-Usher syndrome
 CC or Brazilian pemphigus. An immunostimulator can be used to treat
 CC conditions such as cancer or infection.
 XX
 SQ Sequence 25 AA;

Query Match 98.8%; Score 85; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 8.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
 DB 6 rraavdtycrhnygv 20
 |||||

RESULT 4
 AAR24276
 ID AAR24276 standard; Protein; 89 AA.
 XX
 AC AAR24276;
 DT 19-NOV-1992 (first entry)
 XX
 DE DR1.
 XX
 KW HLA class II; DRB; DQA; DQB; DPB; Hodgkin's disease; multiple sclerosis;
 KW insulin-dependant diabetes.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 3..7
 FT Peptide /label= Polymorphous_region_1
 FT Peptide 21..27
 FT Peptide /label= Polymorphous_region_1
 XX
 XX WO9208117-A.
 XX
 XX 14-MAY-1992.
 XX
 XX 08-OCT-1991; 91WO-US07308.
 XX
 XX 17-OCT-1990; 90NL-0002259.
 XX
 XX (EURO-) EURODIAGNOSTICS BV.
 XX (BIOW) APPLIED BIOSYSTEMS INC.
 XX
 XX Tilanus MG;
 XX
 XX WPI: 1992-183800/22.
 XX N-PSDB; AQ25135.
 XX
 PT Method and kit for determining genotype - by comparing sequences
 PT of gene family members e.g. for disease detection
 XX
 PS Disclosure; Fig 1; 22pp; English.
 XX
 CC The sequence given is an allele of the human DRB locus, DRI. This
 CC allele is distinguishable from other DR alleles by the sequences
 CC contained within the polymorphous regions. These allele specific
 CC oligonucleotides can differ between closely related individuals, see
 CC also AQ25136-45 and AAR24277-86. It can be seen by haplotype analysis
 CC that there are only two distinct DR alleles and the allele specific
 CC oligonucleotides identify different haplotypes.
 CC Sequences from the HLA class II loci DQA, DQB and DPB can also be
 CC analysed to produce similar information. The primer sequences used
 CC in this analysis can be used determining a genotype by comparing the

CC nucleotide sequence of members of a gene system, where the sequences
 CC to be compared are of a strongly conserved section of the genetic
 CC material.
 CC This method can be used to detect genetic variations associated with
 CC diseases or disease symptoms, eg. immune response defects, diseases
 CC associated with the HLA system, such as Hodgkin's disease, multiple
 CC sclerosis and insulin-dependant diabetes. This method may also be
 CC used for tissue or cell typing, eg. to determine the degree of
 CC compatibility of transplants and to determine the risk of an
 CC HLA-associated disease for an animal. It allows the typing of, eg.
 CC HLA class I alleles which could previously only be determined by
 CC serological techniques.
 XX
 SQ Sequence 89 AA;

Query Match 98.8%; Score 85; DB 13; Length 89;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
 DB 66 rraavdtycrhnygv 80
 |||||

RESULT 5
 AAY14343
 ID AAY14343 standard; Protein; 89 AA.
 XX
 AC AAY14343;
 DT 17-AUG-1999 (first entry)
 XX
 DE Protein encoded by HLA-DR beta allele DRW10.
 XX
 KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
 KW major histocompatibility complex; bone marrow transplant; primer;
 KW amplification; polymerase chain reaction; probe; polymorphism;
 KW sequence-specific oligonucleotide probe hybridisation.
 XX
 OS Homo sapiens.
 XX
 XX US5468611-A.
 XX
 XX 21-NOV-1995.
 XX
 XX 08-APR-1993; 93US-0045530.
 XX
 XX 27-JUN-1990; 90US-0544218.
 XX 08-APR-1993; 93US-0045530.
 XX
 XX (BLOO-) BLOOD CENT RES FOUND INC.
 XX
 XX Baxter-Lowe LA, Gorski JA;
 XX
 XX WPI: 1996-010091/01.
 XX N-PSDB; AAX79493.
 XX
 PT Improved method for HLA typing - by DNA amplification and
 PT sequence-specific oligonucleotide hybridisation, used to select
 PT bone marrow donors
 XX
 PS Disclosure; Column 15-16; 20pp; English.
 XX
 CC A novel method of typing the human leukocyte antigen (HLA) of the major
 CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
 CC transplants, involves determining if the donor tissue HLA-DR alleles are
 CC selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,
 CC DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and
 CC DR1a-c (see AAX79451-X79497 for alleles). The method uses PCR to
 CC amplify these regions followed by sequence-specific oligonucleotide
 CC probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH
 CC allows detection of polymorphisms that predict differences at a single

CC amino acid level thus reducing errors and improving the chance of
CC successfully matching tissues. This sequence represents the protein
CC encoded by the HLA-DR allele named in the descriptor line.

XX Sequence 89 AA;

Query Match 98.8%; Score 85; DB 17; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTYCRHNYGV 16
| | | | | | | | | | | | | | | | | |
Db 66 rraavdtycrhnygv 80

RESULT 6
AA14344
ID AAY14344 standard; Protein; 89 AA.

XX AC AAY14344;

DT 17-AUG-1999 (first entry)

DE Protein encoded by HLA-DR beta allele Drla.

XX Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
XX major histocompatibility complex; bone marrow transplant; primer;
XX amplification; polymerase chain reaction; probe; polymorphism;
XX sequence-specific oligonucleotide probe hybridisation.

XX OS Homo sapiens.

XX US5468611-A.

XX 21-NOV-1995.

XX 08-APR-1993; 93US-0045530.

XX 27-JUN-1990; 90US-0544218.

XX 08-APR-1993; 93US-0045530.

XX (BLOO-) BLOOD CENT RES FOUND INC.

XX Baxter-Lowe LA, Gorski JA;

XX WPI; 1996-010091/01.

XX N-PSDB; AAX79494.

XX Improved method for HLA typing - by DNA amplification and
XX sequence-specific oligo:nucleotide hybridisation, used to select
XX bone marrow donors

XX Disclosure; Column 15-16; 20pp; English.

XX A novel method of typing the human leukocyte antigen (HLA) of the major
XX histocompatibility complex (MHC), esp. for typing donors for bone marrow
XX transplants, involves determining if the donor tissue HLA-DR alleles are
XX selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,
XX DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and
XX Drla-c (see AAX79451-X79497 for alleles). The method uses PCR to
XX amplify these regions followed by sequence-specific oligonucleotide
XX probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH
XX allows detection of polymorphisms that predict differences at a single
XX amino acid level thus reducing errors and improving the chance of
XX successfully matching tissues. This sequence represents the protein
XX encoded by the HLA-DR allele named in the descriptor line.

XX Sequence 89 AA;

Query Match 98.8%; Score 85; DB 17; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTYCRHNYGV 16
| | | | | | | | | | | | | | | | | |
Db 66 rraavdtycrhnygv 80

RESULT 7
AA14336
ID AAY14336 standard; Protein; 89 AA.

XX AC AAY14336;

DT 17-AUG-1999 (first entry)

DE Protein encoded by HLA-DR beta allele DR2a/B3.

XX Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
XX major histocompatibility complex; bone marrow transplant; primer;
XX amplification; polymerase chain reaction; probe; polymorphism;
XX sequence-specific oligonucleotide probe hybridisation.

XX OS Homo sapiens.

XX US5468611-A.

XX 21-NOV-1995.

XX 08-APR-1993; 93US-0045530.

XX 27-JUN-1990; 90US-0544218.

XX 08-APR-1993; 93US-0045530.

XX (BLOO-) BLOOD CENT RES FOUND INC.

XX Baxter-Lowe LA, Gorski JA;

XX WPI; 1996-010091/01.

XX N-PSDB; AAX79486.

XX Improved method for HLA typing - by DNA amplification and
XX sequence-specific oligo:nucleotide hybridisation, used to select
XX bone marrow donors

XX Disclosure; Column 15-16; 20pp; English.

XX A novel method of typing the human leukocyte antigen (HLA) of the major
XX histocompatibility complex (MHC), esp. for typing donors for bone marrow
XX transplants, involves determining if the donor tissue HLA-DR alleles are
XX selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,
XX DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and
XX Drla-c (see AAX79451-X79497 for alleles). The method uses PCR to
XX amplify these regions followed by sequence-specific oligonucleotide
XX probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH
XX allows detection of polymorphisms that predict differences at a single
XX amino acid level thus reducing errors and improving the chance of
XX successfully matching tissues. This sequence represents the protein
XX encoded by the HLA-DR allele named in the descriptor line.

XX Sequence 89 AA;

Query Match 98.8%; Score 85; DB 17; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTYCRHNYGV 16
| | | | | | | | | | | | | | | | | |
Db 66 rraavdtycrhnygv 80

RESULT 8
AA14337

ID AAY14337 standard; Protein; 89 AA.
 XX
 AC AAY14337;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Protein encoded by HLA-DR beta allele DR2b/B3.
 XX
 KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
 KW major histocompatibility complex; bone marrow transplant; primer;
 KW amplification; polymerase chain reaction; probe; polymorphism;
 KW sequence-specific oligonucleotide probe hybridisation.
 XX
 OS Homo sapiens.
 XX
 PN US5468611-A.
 XX
 PD 21-NOV-1995.
 XX
 PF 08-APR-1993; 93US-0045530.
 XX
 PR 27-JUN-1990; 90US-0544218.
 PR 08-APR-1993; 93US-0045530.
 XX
 PA (BLOO-) BLOOD CENT RES FOUND INC.
 XX
 PI Baxter-Lowe LA, Gorski JA;
 XX
 DR WPI; 1996-010091/01.
 DR N-PSDB; AAX79487.
 XX
 PT Improved method for HLA typing - by DNA amplification and
 PT sequence-specific oligo:nucleotide hybridisation, used to select
 PT bone marrow donors
 XX
 PS Disclosure; Column 15-16; 20pp; English.
 XX
 CC A novel method of typing the human leukocyte antigen (HLA) of the major
 CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
 CC transplants, involves determining if the donor tissue HLA-DR alleles are
 CC selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,
 CC DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and
 CC DR1a-c (see AAX79451-X79497 for alleles). The method uses PCR to
 CC amplify these regions followed by sequence-specific oligonucleotide
 CC probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH
 CC allows detection of polymorphisms that predict differences at a single
 CC amino acid level thus reducing errors and improving the chance of
 CC successfully matching tissues. This sequence represents the protein
 CC encoded by the HLA-DR allele named in the descriptor line.
 XX
 SQ Sequence 89 AA;
 Query Match 98.8%; Score 85; DB 17; Length 89;
 Best Local Similarity 100.0%; Pred. No. 3.le-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 RRAAVDTYCRHNYGV 16
 Db 66 rraavdtycrhnygv 80
 RESULT 9
 AAY14341
 ID AAY14341 standard; Protein; 89 AA.
 XX
 AC AAY14341;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Protein encoded by HLA-DR beta allele DR2c/B1.
 XX
 KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;

KW major histocompatibility complex; bone marrow transplant; primer;
 KW amplification; polymerase chain reaction; probe; polymorphism;
 KW sequence-specific oligonucleotide probe hybridisation.
 XX
 OS Homo sapiens.
 XX
 PN US5468611-A.
 XX
 PD 21-NOV-1995.
 XX
 PF 08-APR-1993; 93US-0045530.
 XX
 PR 27-JUN-1990; 90US-0544218.
 PR 08-APR-1993; 93US-0045530.
 XX
 PA (BLOO-) BLOOD CENT RES FOUND INC.
 XX
 PI Baxter-Lowe LA, Gorski JA;
 XX
 DR WPI; 1996-010091/01.
 DR N-PSDB; AAX79491.
 XX
 PT Improved method for HLA typing - by DNA amplification and
 PT sequence-specific oligo:nucleotide hybridisation, used to select
 PT bone marrow donors
 XX
 PS Disclosure; Column 15-16; 20pp; English.
 XX
 CC A novel method of typing the human leukocyte antigen (HLA) of the major
 CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
 CC transplants, involves determining if the donor tissue HLA-DR alleles are
 CC selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,
 CC DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and
 CC DR1a-c (see AAX79451-X79497 for alleles). The method uses PCR to
 CC amplify these regions followed by sequence-specific oligonucleotide
 CC probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH
 CC allows detection of polymorphisms that predict differences at a single
 CC amino acid level thus reducing errors and improving the chance of
 CC successfully matching tissues. This sequence represents the protein
 CC encoded by the HLA-DR allele named in the descriptor line.
 XX
 SQ Sequence 89 AA;
 Query Match 98.8%; Score 85; DB 17; Length 89;
 Best Local Similarity 100.0%; Pred. No. 3.le-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 RRAAVDTYCRHNYGV 16
 Db 66 rraavdtycrhnygv 80
 RESULT 10
 AAY14342
 ID AAY14342 standard; Protein; 89 AA.
 XX
 AC AAY14342;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Protein encoded by HLA-DR beta allele DR2d/B1.
 XX
 KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
 KW major histocompatibility complex; bone marrow transplant; primer;
 KW amplification; polymerase chain reaction; probe; polymorphism;
 KW sequence-specific oligonucleotide probe hybridisation.
 XX
 OS Homo sapiens.
 XX
 PN US5468611-A.
 XX
 PD 21-NOV-1995.

```

XX PF 08-APR-1993; 93US-0045530.
XX PR 27-JUN-1990; 90US-0544218.
XX PR 08-APR-1993; 93US-0045530.
XX PA (BLOO-) BLOOD CENT RES FOUND INC.
XX PI Baxter-Lowe LA, Gorski JA;
XX PI
XX DR WPI; 1996-010091/01.
XX DR N-PSDB; AAX79492.
XX
XX PT Improved method for HLA typing - by DNA amplification and
XX PT sequence-specific oligo:nucleotide hybridisation, used to select
XX PT bone marrow donors
XX PS Disclosure; Column 15-16; 20pp; English.
XX
XX CC A novel method of typing the human leukocyte antigen (HLA) of the major
XX CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
XX CC transplants, involves determining if the donor tissue HLA-DR alleles are
XX CC selected from the gp.: HLA-DW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,
XX CC DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and
XX CC DR1a-c (see AAX79451-X79497 for alleles). The method uses PCR to
XX CC amplify these regions followed by sequence-specific oligonucleotide
XX CC probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH
XX CC allows detection of polymorphisms that predict differences at a single
XX CC amino acid level thus reducing errors and improving the chance of
XX CC successfully matching tissues. This sequence represents the protein
XX CC encoded by the HLA-DR allele named in the descriptor line.
XX
XX SQ Sequence 89 AA;

Query Match 98.8%; Score 85; DB 17; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
Db |||||
66 rraavdtcytrhnygv 80

RESULT 11
AAY14329
ID AAY14329 standard; Protein; 89 AA.
XX
XX AC AAY14329;
XX DT 17-AUG-1999 (first entry)
XX DE
XX DE Protein encoded by HLA-DR beta allele DR4b.
XX
XX KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
XX KW major histocompatibility complex; bone marrow transplant; primer;
XX KW amplification; polymerase chain reaction; probe; polymorphism;
XX KW sequence-specific oligonucleotide probe hybridisation.
XX
XX OS Homo sapiens.
XX
XX PN US5468611-A.
XX
XX PD 21-NOV-1995.
XX
XX PF 08-APR-1993; 93US-0045530.
XX PR 27-JUN-1990; 90US-0544218.
XX PR 08-APR-1993; 93US-0045530.
XX PA (BLOO-) BLOOD CENT RES FOUND INC.
XX PI Baxter-Lowe LA, Gorski JA;
XX

```

```

XX
XX DR WPI; 1996-010091/01.
XX DR N-PSDB; AAX79479.
XX
XX PT Improved method for HLA typing - by DNA amplification and
XX PT sequence-specific oligo:nucleotide hybridisation, used to select
XX PT bone marrow donors
XX PS Disclosure; Column 15-16; 20pp; English.
XX
XX CC A novel method of typing the human leukocyte antigen (HLA) of the major
XX CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
XX CC transplants, involves determining if the donor tissue HLA-DR alleles are
XX CC selected from the gp.: HLA-DW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,
XX CC DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and
XX CC DR1a-c (see AAX79451-X79497 for alleles). The method uses PCR to
XX CC amplify these regions followed by sequence-specific oligonucleotide
XX CC probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH
XX CC allows detection of polymorphisms that predict differences at a single
XX CC amino acid level thus reducing errors and improving the chance of
XX CC successfully matching tissues. This sequence represents the protein
XX CC encoded by the HLA-DR allele named in the descriptor line.
XX
XX SQ Sequence 89 AA;

Query Match 98.8%; Score 85; DB 17; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
Db |||||
66 rraavdtcytrhnygv 80

RESULT 12
AAY14332
ID AAY14332 standard; Protein; 89 AA.
XX
XX AC AAY14332;
XX DT 17-AUG-1999 (first entry)
XX DE
XX DE Protein encoded by HLA-DR beta allele DR4e.
XX
XX KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
XX KW major histocompatibility complex; bone marrow transplant; primer;
XX KW amplification; polymerase chain reaction; probe; polymorphism;
XX KW sequence-specific oligonucleotide probe hybridisation.
XX
XX OS Homo sapiens.
XX
XX PN US5468611-A.
XX
XX PD 21-NOV-1995.
XX
XX PF 08-APR-1993; 93US-0045530.
XX PR 27-JUN-1990; 90US-0544218.
XX PR 08-APR-1993; 93US-0045530.
XX PA (BLOO-) BLOOD CENT RES FOUND INC.
XX PI Baxter-Lowe LA, Gorski JA;
XX
XX DR WPI; 1996-010091/01.
XX DR N-PSDB; AAX79482.
XX
XX PT Improved method for HLA typing - by DNA amplification and
XX PT sequence-specific oligo:nucleotide hybridisation, used to select
XX PT bone marrow donors
XX PS Disclosure; Column 15-16; 20pp; English.

```

XX A novel method of typing the human leukocyte antigen (HLA) of the major
 CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
 CC transplants, involves determining if the donor tissue HLA-DR alleles are
 CC selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,
 CC DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and
 CC DR1a-c (see AAX79451-X79497 for alleles). The method uses PCR to
 CC amplify these regions followed by sequence-specific oligonucleotide
 CC probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH
 CC allows detection of polymorphisms that predict differences at a single
 CC amino acid level thus reducing errors and improving the chance of
 CC successfully matching tissues. This sequence represents the protein
 CC encoded by the HLA-DR allele named in the descriptor line.

XX Sequence 89 AA;
 SQ

Query Match 98.8%; Score 85; DB 17; Length 89;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTYCRHNYGV 16
 |||||
 Db 66 rraavdtycrhnygv 80

RESULT 13
 AAY14310
 ID AAY14310 standard; Protein; 89 AA.
 XX
 AC AAY14310;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Protein encoded by HLA-DR beta allele DR5a.
 XX
 KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
 KW major histocompatibility complex; bone marrow transplant; primer;
 KW amplification; polymerase chain reaction; probe; polymorphism;
 KW sequence-specific oligonucleotide probe hybridisation.

XX Homo sapiens.
 XX US5468611-A.
 XX
 PD 21-NOV-1995.
 XX
 PF 08-APR-1993; 93US-0045530.
 XX
 PR 27-JUN-1990; 90US-0544218.
 PR 08-APR-1993; 93US-0045530.
 XX
 PA (BLOO-) BLOOD CENT RES FOUND INC.
 XX
 PI Baxter-Lowe LA, Gorski JA;
 XX
 DR WPI; 1996-010091/01.
 DR N-PSDB; AAX79460.
 XX
 PT Improved method for HLA typing - by DNA amplification and
 PT sequence-specific oligo:nucleotide hybridisation, used to select
 PT bone marrow donors
 XX
 PS Disclosure; Column 15-16; 20pp; English.

XX A novel method of typing the human leukocyte antigen (HLA) of the major
 CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
 CC transplants, involves determining if the donor tissue HLA-DR alleles are
 CC selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,
 CC DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and
 CC DR1a-c (see AAX79451-X79497 for alleles). The method uses PCR to
 CC amplify these regions followed by sequence-specific oligonucleotide
 CC probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH
 CC allows detection of polymorphisms that predict differences at a single
 CC amino acid level thus reducing errors and improving the chance of
 CC successfully matching tissues. This sequence represents the protein
 CC encoded by the HLA-DR allele named in the descriptor line.

XX allows detection of polymorphisms that predict differences at a single
 CC amino acid level thus reducing errors and improving the chance of
 CC successfully matching tissues. This sequence represents the protein
 CC encoded by the HLA-DR allele named in the descriptor line.

XX Sequence 89 AA;
 SQ

Query Match 98.8%; Score 85; DB 17; Length 89;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAAVDTYCRHNYGV 16
 |||||
 Db 66 rraavdtycrhnygv 80

RESULT 14
 AAY14314
 ID AAY14314 standard; Protein; 89 AA.
 XX
 AC AAY14314;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Protein encoded by HLA-DR beta allele DR5e.
 XX
 KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
 KW major histocompatibility complex; bone marrow transplant; primer;
 KW amplification; polymerase chain reaction; probe; polymorphism;
 KW sequence-specific oligonucleotide probe hybridisation.

XX Homo sapiens.
 XX US5468611-A.
 XX
 PD 21-NOV-1995.
 XX
 PF 08-APR-1993; 93US-0045530.
 XX
 PR 27-JUN-1990; 90US-0544218.
 PR 08-APR-1993; 93US-0045530.
 XX
 PA (BLOO-) BLOOD CENT RES FOUND INC.
 XX
 PI Baxter-Lowe LA, Gorski JA;
 XX
 DR WPI; 1996-010091/01.
 DR N-PSDB; AAX79464.
 XX
 PT Improved method for HLA typing - by DNA amplification and
 PT sequence-specific oligo:nucleotide hybridisation, used to select
 PT bone marrow donors
 XX
 PS Disclosure; Column 15-16; 20pp; English.

XX A novel method of typing the human leukocyte antigen (HLA) of the major
 CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
 CC transplants, involves determining if the donor tissue HLA-DR alleles are
 CC selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,
 CC DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and
 CC DR1a-c (see AAX79451-X79497 for alleles). The method uses PCR to
 CC amplify these regions followed by sequence-specific oligonucleotide
 CC probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH
 CC allows detection of polymorphisms that predict differences at a single
 CC amino acid level thus reducing errors and improving the chance of
 CC successfully matching tissues. This sequence represents the protein
 CC encoded by the HLA-DR allele named in the descriptor line.

XX Sequence 89 AA;
 SQ

Query Match 98.8%; Score 85; DB 17; Length 89;

Search completed: July 1, 2002, 12:20:08
Job time: 225 sec

Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
| | | | | | | | | | | | | | | |
Db 66 rraavdtycrhnygv 80

RESULT 15

AAV14319
ID AAY14319 standard; Protein; 89 AA.

XX AC AAY14319;

XX DT 17-AUG-1999 (first entry)

XX DE Protein encoded by HLA-DR beta allele DRW6d.

XX KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
KW major histocompatibility complex; bone marrow transplant; primer;
KW amplification; polymerase chain reaction; probe; polymorphism;
KW sequence-specific oligonucleotide probe hybridisation.

XX OS Homo sapiens.

XX PN US5468611-A.

XX PD 21-NOV-1995.

XX PF 08-APR-1993; 93US-0045530.

XX PR 27-JUN-1990; 90US-0544218.

XX PR 08-APR-1993; 93US-0045530.

XX PA (BLOO-) BLOOD CENT RES FOUND INC.

XX PI Baxter-Lowe LA, Gorski JA;

XX DR WPI; 1996-010091/01.

XX DR N-PSDB; AAX79469.

XX PT Improved method for HLA typing - by DNA amplification and
PT sequence-specific oligo:nucleotide hybridisation, used to select
PT bone marrow donors

XX PS Disclosure; Column 15-16; 20pp; English.

XX CC A novel method of typing the human leukocyte antigen (HLA) of the major
CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
CC transplants, involves determining if the donor tissue HLA-DR alleles are
CC selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1,
CC DR6a, DR8a-d, DRW63a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and
CC DR1a-c (see AAX79451-X79497 for alleles). The method uses PCR to
CC amplify these regions followed by sequence-specific oligonucleotide
CC probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH
CC allows detection of polymorphisms that predict differences at a single
CC amino acid level thus reducing errors and improving the chance of
CC successfully matching tissues. This sequence represents the protein
CC encoded by the HLA-DR allele named in the descriptor line.

XX SQ Sequence 89 AA;

Query Match 98.8%; Score 85; DB 17; Length 89;

Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAAVDTYCRHNYGV 16
| | | | | | | | | | | | | | | |
Db 66 rraavdtycrhnygv 80

